

SEQUENCE LISTING

- 5 (1) GENERAL INFORMATION:
- 10 (i) APPLICANTS: Kendall, Richard L.
Thomas, Kenneth A.
Mao, Xianzhi
Tebben, Andrew J.
- (ii) TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
- 15 (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
20 (A) ADDRESSEE: Merck & Co., Inc.
(B) STREET: P.O. Box 2000
(C) CITY: Rahway
(D) STATE: NJ
(E) COUNTRY: US
(F) ZIP: 07065-0907
- 25 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 30 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- 35 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Hand, J. Mark
(B) REGISTRATION NUMBER: 36,545
(C) REFERENCE/DOCKET NUMBER: 19963PV
- 40 (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 732/594-3905
(B) TELEFAX: 732/594-4720
- 45 (2) INFORMATION FOR SEQ ID NO:1:
- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4071 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 ATGGAGAGCA AGGTGCTGCT GGCCGTCGCC CTGTGGCTCT GCGTGGAGAC CCGGGCCGCC 60
 TCTGTGGGTT TGCCTAGTGT TTCTCTTGAT CTGCCCAGGC TCAGCATACA AAAAGACATA 120
 CTTACAATTA AGGCTAATAC AACTCTTCAA ATTACTTGCA GGGGACAGAG GGACTTGGAC 180
 10 TGGCTTTGGC CCAATAATCA GAGTGGCAGT GAGCAAAGGG TGGAGGTGAC TGAGTGCAGC 240
 GATGGCCTCT TCTGTAAGAC ACTCACAATT CCAAAGTGA TCGGAAATGA CACTGGAGCC 300
 TACAAGTGCT TCTACCGGGA AACTGACTTG GCCTCGGTCA TTTATGTCTA TGTTCAAGAT 360
 15 TACAGATCTC CATTTATTGC TTCTGTTAGT GACCAACATG GAGTCGTGTA CATTACTGAG 420
 AACAAAAACA AAAGTGTGGT GATTCCATGT CTCGGGTCCA TTCAAATCT CAACGTGTCA 480
 CTTGTGCAA GATACCCAGA AAAGAGATT GTTCCTGATG GTAACAGAAT TTCCTGGGAC 540
 20 AGCAAGAAGG GCTTTACTAT TCCCAGCTAC ATGATCAGCT ATGCTGGCAT GGTCTTCTGT 600
 GAAGCAAAAA TTAATGATGA AAGTTACCAG TCTATTATGT ACATAGTTGT CGTTGTAGGG 660
 25 TATAGGATTT ATGATGTGGT TCTGAGTCCG TCTCATGGAA TTGAACTATC TGTGGAGAA 720
 AAGCTTGTCT TAAATTGTAC AGCAAGAACT GAACTAAATG TGGGGATTGA CTTCAACTGG 780
 GAATACCCTT CTTGGAAGCA TCAGCATAAG AAAGTTGTAA ACCGAGACCT AAAAACCAG 840
 30 TCTGGGAGTG AGATGAAGAA ATTTTGTAGC ACCTTAACTA TAGATGGTGT AATCCGGAGT 900
 GACCAAGGAT TGTACACCTG TGCAGCATCC AGTGGGCTGA TGACCAAGAA GAACAGCACA 960
 35 TTTGTCAGGG TCCATGAAAA ACCTTTTGTG GCTTTTGGAA GTGGCATGGA ATCTCTGGTG 1020
 GAAGCCACGG TGGGGGAGCG TGTCAGAATC CCTGCGAAGT ACCTTGGTTA CCCACCCCCA 1080
 GAAATAAAAT GGTATAAAAA TGGAATACCC CTTGAGTCCA ATCACACAAT TAAAGCGGGG 1140
 40 CATGTACTGA CGATTATGGA AGTGAGTGAA AGAGACACAG GAAATTACAC TGTCATCCTT 1200
 ACCAATCCCA TTTCAAAGGA GAAGCAGAGC CATGTGGTCT CTCTGGTTGT GTATGTCCCA 1260
 45 CCCAGATTG GTGAGAAATC TCTAATCTCT CCTGTGGATT CCTACCAGTA CGGCACCACT 1320
 CAAACGCTGA CATGTACGGT CTATGCCATT CCTCCCCCGC ATCACATCCA CTGGTATTGG 1380
 CAGTTGGAGG AAGAGTGGCG CAACGAGCCC AGCCAAGCTG TCTCAGTGAC AAACCCATAC 1440
 50 CCTGTGAAG AATGGAGAAG TGTGGAGGAC TTCCAGGGAG GAAATAAAAT TGAAGTTAAT 1500
 AAAAAATCAAT TTGCTCTAAT TGAAGGAAAA AACAAAATG TAAGTACCCT TGTTATCCAA 1560
 55 GCGCAAATG TGTCAGCTTT GTACAAATGT GAAGCGGTCA ACAAAGTCGG GAGAGGAGAG 1620
 AGGGTGATCT CCTTCCACGT GACCAGGGGT CCTGAAATTA CTTTGCAACC TGACATGCAG 1680

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	CCCACTGAGC	AGGAGAGCGT	GTCTTTGTGG	TGCACTGCAG	ACAGATCTAC	GTTTGAGAAC	1740
	CTCACATGGT	ACAAGCTTGG	CCCACAGCCT	CTGCCAATCC	ATGTGGGAGA	GTTGCCCACA	1800
5	CCTGTTTGCA	AGAACTTGGA	TACTCTTTGG	AAATTGAATG	CCACCATGTT	CTCTAATAGC	1860
	ACAAATGACA	TTTTGATCAT	GGAGCTTAAG	AATGCATCCT	TGCAGGACCA	AGGAGACTAT	1920
10	GTCTGCCTTG	CTCAAGACAG	GAAGACCAAG	AAAAGACATT	GCGTGGTCAG	GCAGCTCACA	1980
	GTCTTAGAGC	GTGTGGCACC	CACGATCACA	GGAAACCTGG	AGAATCAGAC	GACAAGTATT	2040
	GGGGAAAGCA	TCGAAGTCTC	ATGCACGGCA	TCTGGGAATC	CCCCTCCACA	GATCATGTGG	2100
15	TTTAAAGATA	ATGAGACCCT	TGTAGAAGAC	TCAGGCATTG	TATTGAAGGA	TGGGAACCGG	2160
	AACCTCACTA	TCCGCAGAGT	GAGGAAGGAG	GACGAAGGCC	TCTACACCTG	CCAGGCATGC	2220
20	AGTGTTCCTG	GCTGTGCAAA	AGTGGAGGCA	TTTTTCATAA	TAGAAGGTGC	CCAGGAAAAG	2280
	ACGAACTTGG	AAATCATTAT	TCTAGTAGGC	ACGGCGGTGA	TTGCCATGTT	CTTCTGGCTA	2340
	CTTCTTGTC	TCATCCTACG	GACCGTTAAG	CGGGCCAATG	GAGGGGAACT	GAAGACAGGG	2400
25	TACCTGTCCA	TCGTCATGGA	TCCAGATGAA	CTCCCATTTG	ATGAACATTG	TGAACGACTG	2460
	CCTTATGATG	CCAGCAAATG	GGAATTCCCC	AGAGACCGGC	TGAAGCTAGG	TAAGCCTCTT	2520
30	GGCCGTGGTG	CCTTTGGCCA	AGTGATTGAA	GCAGATGCCT	TTGGAATTGA	CAAGACAGCA	2580
	ACTTGCAGGA	CAGTAGCAGT	CAAAATGTTG	AAAGAAGGAG	CAACACACAG	TGAGCATCGA	2640
	GCTCTCATGT	CTGAACTCAA	GATCCTCATT	CATATTGGTC	ACCATCTCAA	TGTGGTCAAC	2700
35	CTTCTAGGTG	CCTGTACCAA	GCCAGGAGGG	CCACTCATGG	TGATTGTGGA	ATTCTGCAAA	2760
	TTTGGAACC	TGTCCACTTA	CCTGAGGAGC	AAGAGAAATG	AATTTGTCCC	CTACAAGACC	2820
40	AAAGGGGCAC	GATTCCGTCA	AGGGAAAGAC	TACGTTGGAG	CAATCCCTGT	GGATCTGAAA	2880
	CGGCGCTTGG	ACAGCATCAC	CAGTAGCCAG	AGCTCAGCCA	GCTCTGGATT	TGTGGAGGAG	2940
	AAGTCCCTCA	GTGATGTAGA	AGAAGAGGAA	GCTCCTGAAG	ATCTGTATAA	GGACTTCCTG	3000
45	ACCTTGGAGC	ATCTCATCTG	TTACAGCTTC	CAAGTGGCTA	AGGGCATGGA	GTTCTTGGCA	3060
	TCGCGAAAGT	GTATCCACAG	GGACCTGGCG	GCACGAAATA	TCCTCTTATC	GGAGAAGAAC	3120
50	GTGGTTAAAA	TCTGTGACTT	TGGCTTGGCC	CGGGATATTT	ATAAAGATCC	AGATTATGTC	3180
	AGAAAAGGAG	ATGCTCGCCT	CCCTTTGAAA	TGGATGGCCC	CAGAAACAAT	TTTTGACAGA	3240
	GTGTACACAA	TCCAGAGTGA	CGTCTGGTCT	TTTGGTGTTT	TGCTGTGGGA	AATATTTTCC	3300
55	TTAGGTGCTT	CTCCATATCC	TGGGGTAAAG	ATTGATGAAG	AATTTTGTAG	GCGATTGAAA	3360
	GAAGGAACTA	GAATGAGGGC	CCCTGATTAT	ACTACACCAG	AAATGTACCA	GACCATGCTG	3420

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GACTGCTGGC ACGGGGAGCC CAGTCAGAGA CCCACGTTTT CAGAGTTGGT GGAACATTTG 3480
 GGAAATCTCT TGCAAGCTAA TGCTCAGCAG GATGGCAAAG ACTACATTGT TCTTCCGATA 3540
 5 TCAGAGACTT TGAGCATGGA AGAGGATTCT GGACTCTCTC TGCCTACCTC ACCTGTTTCC 3600
 TGTATGGAGG AGGAGGAAGT ATGTGACCCC AAATTCCATT ATGACAACAC AGCAGGAATC 3660
 10 AGTCAGTATC TGCAGAACAG TAAGCGAAAG AGCCGGCCTG TGAGTGTAAG AACATTTGAA 3720
 GATATCCCGT TAGAAGAACC AGAAGTAAAA GTAATCCCAG ATGACAACCA GACGGACAGT 3780
 GGTATGGTTC TTGCCTCAGA AGAGCTGAAA ACTTTGGAAG ACAGAACCAA ATTATCTCCA 3840
 15 TCTTTTGGTG GAATGGTGCC CAGCAAAAGC AGGGAGTCTG TGGCATCTGA AGGCTCAAAC 3900
 CAGACAAGCG GCTACCAGTC CGGATATCAC TCCGATGACA CAGACACCAC CGTGTACTCC 3960
 AGTGAGGAAG CAGAACTTTT AAAGCTGATA GAGATTGGAG TGCAAACCGG TAGCACAGCC 4020
 20 CAGATTCTCC AGCCTGACTC GGGGACCACA CTGAGCTCTC CTCCTGTTTA A 4071

(2) INFORMATION FOR SEQ ID NO:2:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1356 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
 1 5 10 15
 35 Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
 20 25 30
 40 Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
 35 40 45
 Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
 50 55 60
 45 Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
 65 70 75 80
 50 Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
 85 90 95
 Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
 100 105 110
 55 Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
 115 120 125
 Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
 130 135 140

	Thr	Val	Val	Ile	Pro	Cys	Leu	Gly	Ser	Ile	Ser	Asn	Leu	Asn	Val	Ser	
	145					150					155					160	
5	Leu	Cys	Ala	Arg	Tyr	Pro	Glu	Lys	Arg	Phe	Val	Pro	Asp	Gly	Asn	Arg	
					165					170					175		
	Ile	Ser	Trp	Asp	Ser	Lys	Lys	Gly	Phe	Thr	Ile	Pro	Ser	Tyr	Met	Ile	
10				180					185					190			
	Ser	Tyr	Ala	Gly	Met	Val	Phe	Cys	Glu	Ala	Lys	Ile	Asn	Asp	Glu	Ser	
			195					200					205				
15	Tyr	Gln	Ser	Ile	Met	Tyr	Ile	Val	Val	Val	Val	Gly	Tyr	Arg	Ile	Tyr	
	210						215					220					
	Asp	Val	Val	Leu	Ser	Pro	Ser	His	Gly	Ile	Glu	Leu	Ser	Val	Gly	Glu	
	225					230					235					240	
20	Lys	Leu	Val	Leu	Asn	Cys	Thr	Ala	Arg	Thr	Glu	Leu	Asn	Val	Gly	Ile	
					245					250					255		
	Asp	Phe	Asn	Trp	Glu	Tyr	Pro	Ser	Ser	Lys	His	Gln	His	Lys	Lys	Leu	
25				260					265					270			
	Val	Asn	Arg	Asp	Leu	Lys	Thr	Gln	Ser	Gly	Ser	Glu	Met	Lys	Lys	Phe	
			275					280					285				
30	Leu	Ser	Thr	Leu	Thr	Ile	Asp	Gly	Val	Thr	Arg	Ser	Asp	Gln	Gly	Leu	
	290						295					300					
	Tyr	Thr	Cys	Ala	Ala	Ser	Ser	Gly	Leu	Met	Thr	Lys	Lys	Asn	Ser	Thr	
	305					310					315					320	
35	Phe	Val	Arg	Val	His	Glu	Lys	Pro	Phe	Val	Ala	Phe	Gly	Ser	Gly	Met	
					325					330					335		
	Glu	Ser	Leu	Val	Glu	Ala	Thr	Val	Gly	Glu	Arg	Val	Arg	Ile	Pro	Ala	
40				340					345					350			
	Lys	Tyr	Leu	Gly	Tyr	Pro	Pro	Pro	Glu	Ile	Lys	Trp	Tyr	Lys	Asn	Gly	
			355					360					365				
45	Ile	Pro	Leu	Glu	Ser	Asn	His	Thr	Ile	Lys	Ala	Gly	His	Val	Leu	Thr	
	370						375					380					
	Ile	Met	Glu	Val	Ser	Glu	Arg	Asp	Thr	Gly	Asn	Tyr	Thr	Val	Ile	Leu	
	385					390					395					400	
50	Thr	Asn	Pro	Ile	Ser	Lys	Glu	Lys	Gln	Ser	His	Val	Val	Ser	Leu	Val	
					405					410						415	
	Val	Tyr	Val	Pro	Pro	Gln	Ile	Gly	Glu	Lys	Ser	Leu	Ile	Ser	Pro	Val	
				420					425					430			
55	Asp	Ser	Tyr	Gln	Tyr	Gly	Thr	Thr	Gln	Thr	Leu	Thr	Cys	Thr	Val	Tyr	
			435					440					445				

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Ala Ile Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu
 450 455 460
 5 Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
 465 470 475 480
 Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys
 485 490 495
 10 Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys
 500 505 510
 Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
 515 520 525
 15 Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser
 530 535 540
 20 Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln
 545 550 555 560
 Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser
 565 570 575
 25 Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro
 580 585 590
 Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr
 595 600 605
 30 Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile
 610 615 620
 Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr
 625 630 635 640
 35 Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val
 645 650 655
 40 Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn
 660 665 670
 Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys
 675 680 685
 45 Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn
 690 695 700
 50 Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg
 705 710 715 720
 Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr
 725 730 735
 55 Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe
 740 745 750

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	Ile	Ile	Glu	Gly	Ala	Gln	Glu	Lys	Thr	Asn	Leu	Glu	Ile	Ile	Ile	Leu
			755					760					765			
5	Val	Gly	Thr	Ala	Val	Ile	Ala	Met	Phe	Phe	Trp	Leu	Leu	Leu	Val	Ile
		770					775					780				
	Ile	Leu	Arg	Thr	Val	Lys	Arg	Ala	Asn	Gly	Gly	Glu	Leu	Lys	Thr	Gly
	785					790					795					800
10	Tyr	Leu	Ser	Ile	Val	Met	Asp	Pro	Asp	Glu	Leu	Pro	Leu	Asp	Glu	His
					805					810					815	
	Cys	Glu	Arg	Leu	Pro	Tyr	Asp	Ala	Ser	Lys	Trp	Glu	Phe	Pro	Arg	Asp
				820					825					830		
15	Arg	Leu	Lys	Leu	Gly	Lys	Pro	Leu	Gly	Arg	Gly	Ala	Phe	Gly	Gln	Val
			835					840					845			
20	Ile	Glu	Ala	Asp	Ala	Phe	Gly	Ile	Asp	Lys	Thr	Ala	Thr	Cys	Arg	Thr
	850						855					860				
	Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Gly	Ala	Thr	His	Ser	Glu	His	Arg
	865					870					875					880
25	Ala	Leu	Met	Ser	Glu	Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	His	His	Leu
					885				890					895		
	Asn	Val	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Lys	Pro	Gly	Gly	Pro	Leu
				900					905					910		
30	Met	Val	Ile	Val	Glu	Phe	Cys	Lys	Phe	Gly	Asn	Leu	Ser	Thr	Tyr	Leu
		915						920					925			
35	Arg	Ser	Lys	Arg	Asn	Glu	Phe	Val	Pro	Tyr	Lys	Thr	Lys	Gly	Ala	Arg
		930					935					940				
	Phe	Arg	Gln	Gly	Lys	Asp	Tyr	Val	Gly	Ala	Ile	Pro	Val	Asp	Leu	Lys
	945					950					955					960
40	Arg	Arg	Leu	Asp	Ser	Ile	Thr	Ser	Ser	Gln	Ser	Ser	Ala	Ser	Ser	Gly
					965					970					975	
	Phe	Val	Glu	Glu	Lys	Ser	Leu	Ser	Asp	Val	Glu	Glu	Glu	Glu	Ala	Pro
				980					985					990		
45	Glu	Asp	Leu	Tyr	Lys	Asp	Phe	Leu	Thr	Leu	Glu	His	Leu	Ile	Cys	Tyr
		995						1000					1005			
50	Ser	Phe	Gln	Val	Ala	Lys	Gly	Met	Glu	Phe	Leu	Ala	Ser	Arg	Lys	Cys
		1010					1015					1020				
	Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Leu	Ser	Glu	Lys	Asn
	1025					1030					1035					1040
55	Val	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Tyr	Lys	Asp
					1045					1050					1055	

5 Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met
 1060 1065 1070
 Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val
 1075 1080 1085
 Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser
 1090 1095 1100
 10 Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys
 1105 1110 1115 1120
 Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro Glu Met Tyr
 1125 1130 1135
 15 Gln Thr Met Leu Asp Cys Trp His Gly Glu Pro Ser Gln Arg Pro Thr
 1140 1145 1150
 Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala
 1155 1160 1165
 20 Gln Gln Asp Gly Lys Asp Tyr Ile Val Leu Pro Ile Ser Glu Thr Leu
 1170 1175 1180
 Ser Met Glu Glu Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser
 1185 1190 1195 1200
 25 Cys Met Glu Glu Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn
 1205 1210 1215
 30 Thr Ala Gly Ile Ser Gln Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg
 1220 1225 1230
 Pro Val Ser Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu
 1235 1240 1245
 35 Val Lys Val Ile Pro Asp Asp Asn Gln Thr Asp Ser Gly Met Val Leu
 1250 1255 1260
 40 Ala Ser Glu Glu Leu Lys Thr Leu Glu Asp Arg Thr Lys Leu Ser Pro
 1265 1270 1275 1280
 Ser Phe Gly Gly Met Val Pro Ser Lys Ser Arg Glu Ser Val Ala Ser
 1285 1290 1295
 45 Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp
 1300 1305 1310
 50 Asp Thr Asp Thr Thr Val Tyr Ser Ser Glu Glu Ala Glu Leu Leu Lys
 1315 1320 1325
 Leu Ile Glu Ile Gly Val Gln Thr Gly Ser Thr Ala Gln Ile Leu Gln
 1330 1335 1340
 55 Pro Asp Ser Gly Thr Thr Leu Ser Ser Pro Pro Val
 1345 1350 1355

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAATTCCAT CCAAGCGGCA AATGTGTC

28

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGAATTCCGA GTCTTCTACA AGGGTCTC

28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTATGACAAC ACAGCAGG

18

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5 TTGGATCCTC GAGTTGGGGT GTGGATGC

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20 GGATCCAGAT GAACTCCCAT TG

22

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

35 GTCGACTTAG TCTTTGCCAT CCTGCTGAGC

30

40